



QY 263 QNLLSGGIYPTKPPGDPMPMPNQPOQTTSVLRKVAIDYISK----- 305  
 Db 481 D-----VNTEKELT-----DVTNOYLOKITYGDNNSAVDFNADSAVYVMN 522  
 QY 306 -----LLEGATIQLTGD----- 319  
 Db 523 TKFQINTNSESPTLWQMATLSSTGKVSYSTGNALGFTNNQSGAGQEVYVIGNYWEDTIN 582  
 QY 320 NSFO-----ARVSSN---DIGERIELSDGTYLTTEL-----NSPAGS 355  
 Db 583 NGVQBLGERGVGNVTVTVDNTNTWKVGAVTKEDGSYLLPNLNGDYRVEFSNLPGKE 642  
 QY 356 IAE----- 358  
 Db 643 VTPSKQGNNEELDSNGLSSVTNGKDNLSADLGTYKPKYNLSDYVWEDTNKNGIODE 702  
 QY 359 -----PIFKVEAGKVY-----TIIDGK---QIENPNKEI-----WEPSVSEAYNDF 397  
 Db 703 KGISCVTWTIKDENGVLTVTADGKFKTDLNGNKTVEFTTPEGTTPTVTSGR 762  
 QY 398 EEF-S-VLTTONY-----AKPYYAKNKGSSQVVCNFNADLKSPPDSED---GGKT 443  
 Db 763 EKDSNLTTGTINGADNMTLDGSFVYKTKYKINLGNYVWEDTNKDGQ---DSTERGISGVT 820  
 QY 444 MTPPTTGVYKTHLAGR-LFKTYVKPDTDPDTFLKIKVIEKGQALIEY--- 499  
 Db 821 VTLKNENGEVLTQTKDQKGQYI-----GLNGTYKVEFEP 859  
 Qy 500 SGLTETQLAATQALI-YIFTDSAELDK-----LKDY-----HGFG 536  
 Db 860 SGYPTPTQVSGTDBGIDSNNGTSTTGVIKDKNDTDSGFYKPTVNLGDYVWEDTNKNGQ 919  
 QY 537 DMNSTLAVA-----KILVEYAQDSNPP-OLTDLDFIPNNKQSLIGTQWHPED 586  
 Db 920 DKDEKGISCVTWTIKDENGVLTVTADGKFKTDL-----NNCTYK----- 963  
 QY 587 LVDITRMERKEVTP-VHNLTLRK-----TVYGL---AGDRKDFHEIELKNKQBL 636  
 Db 964 ---VEFEPSPGYPTSVTSGNDTEKDSNGLITGVIKDADNMTLDGF---VTPKYS 1016  
 QY 637 -----LSQTVKDQTKNEFQCKATINLKHGSLSITQGLPCESYLSVYKETSEGYK 689  
 Db 1017 GDYWWYDSNRKGKODSTERKGIVKVTLINEKEVGIVTGTDTENGKCPDNLDGSKYKV 1076  
 QY 690 VNSQEVANAVSKIGTSSETLAFENKKEPVVPTGVQDKI-NGY 732  
 Db 1077 F-EKPAGLQTGTNTTEDKDADGGEVYVITDHDFILDNGY 1118

RESULT 2

US-10-615-383-10  
 ; Sequence 10, Application US/10615383  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FOSNER, Timothy  
 ; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES FROM COAGULASE-NEGATIVE STAPHYLC  
 ; FILE REFERENCE: P0635US03/BAS  
 ; CURRENT APPLICATION NUMBER: US/10-615, 383  
 ; CURRENT FILING DATE: 2003-07-09  
 ; PRIOR APPLICATION NUMBER: 09-3786, 962  
 ; PRIOR FILING DATE: 1999-08-31  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 10  
 ; LENGTH: 930  
 ; TYPE: PPT  
 ; ORGANISM: Staphylococcus epidermidis  
 ; US-10-615-383-10

Query Match 3.68; Score 142; DB 6; Length 930;

Best Local Similarity 18.6%; Pred. No. 0.039; Matches 161; Conservative 131; Mismatches 295; Indels 278; Gaps 42;

Matches 161; Conservative 131; Mismatches 295; Indels 278; Gaps 42;

QY 9 KLNINTQ---VLSKNSK---RTVTIUVFLMIALVTSMQAKTVFGL---VES 56  
 Db 2 KKNNLTKKPKIANNSNKAIKRTVGTASI-----VIGAALFGLGHNKAEE 51  
 QY 57 STPNAIAPDSSEVYKWWYQYESVYRQHYYKQFRVADLVRNLECGSSRYOVCENLKKAPP 116  
 Db 52 NTQDVK-DSND-----DELSNSDOSSNEERK---VNNQSIN 89  
 QY 117 LGSPSSVK-WKKHDGISKTFEDYAMS-----PRITGDELNOKLRVWMYH 163  
 Db 90 TDDDNQIKKEETNSNDAIENRSKDTQSTINVDNEATFLQKTPQDNTFOLKEEVVKEPSS 149  
 QY 164 PONANGIMECLEPLNAINRITQEAQWYVSNAPN-S-PDESFKRESESNUVTSQLSLRQ 222  
 Db 150 VENNSMMAQDQSHTTINSEASITQNTSEENNSRVSDFANSKLTIESNTNEEINT 209  
 Db 223 ALKQLDIPNLATMKRQVDPDFQLSIFESBDKGKYNQYQNLISGGLVPTKPTPGDP 282  
 Db 210 -----PKVREDSITSQSSYKNDKEKISQDELL--LPINSEYENKVRP 252  
 QY 283 MPPN---QPOITSVLRKLYIGDYSKLLCATLQIYGDYNNNSFOARFESSNDIGERIELSD 340  
 Db 253 LSTNSAQPSSKRVTVNOLAEO-----GSNVNHLIK-VTQD SITEGYDSD 297  
 QY 341 GTYVITELNSPAGYSSAEPITKVEAGKVYI-TDGKQI----- 378  
 Db 298 GTKRAHDAENLI-IVTVEFUDKQGDMTNVNDKNTVPSDLJDSFAIPKIKDNGHII 356  
 QY 379 -----ENPNEIKEVEFYS-VEAYNDFEEFESVLTQNTQYAKFYYAKN-NGSSQVYCNA 429  
 Db 357 ATGTYDNTNKOQITYFTDQVYKVNENIKAIKLT-----YDTSKVPNNTKLDEVT 410  
 QY 430 DLKSEPDSEGGKINTPDPF-----TTGEVK-YTHIACRDLKRYTVPRTDTPDTFLK 481  
 Db 411 ALSSV-----NKSTTVEQKPNERNNTANLQSMETI--DTKNHIV---EQTYINP 456  
 QY 482 IKVIEKGYREKGAAIEVGSLTE--TOLRAATOLAIYFTDRAEL-DKDKLKDQHGGD 537  
 Db 457 LR-----SAKETVNNTLNGNGDEGSTIDSTIHKVKGDMQNLPSNRYTDESEED 510  
 Qy 538 MNDSTLAVAKILVEYAQDSNPPQLTDLDFIPNNKQYSLIGTQWHPEDLVIMED- 595  
 Db 511 VTND-----DYAQ-----LGNNNDVNINFGNIDSPY-IKIVSKYDPN 547  
 QY 596 KKEVTPVTHNLTLRKTVTGLAD----- 626  
 Db 548 KDDTTIQTQVTMOTNTNEYTGERTASYDNTIAFSTSSQGQGDLPPEKTYKIGDYWE 607  
 QY 627 -----IELKNNKQBL-----SQTVKTDKUNLEFRDGKATINLKH---ESL 665  
 Db 608 DVDKDQGQIQTNDNEKPLSNAVLVITYPDGTSKSYRTRDEBGKQFQDG---LKNGLYKI 662  
 QY 666 TQGSPGEGSYSLVKET-----DSEGVYKVNQSEVANAT----- 700  
 Db 663 TEE-TPEGYTPTLKHSGTNPALPSEGNSWVTINGQDDMTIDSGFYOPTPKYSLGNVYWW 721  
 QY 701 -SKIGITSD-----TLAEN 715  
 Db 722 TNKDGQIQCDEKGISGVKVTLDEN 746

RESULT 3

US-10-617-320-3676  
 ; Sequence 3676, Application US/10617320  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lynn A Doucette-Staam and David Bush  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIA  
 ; NUMBER OF SEQUENCES: 5206

## CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street

CITY: Waltham

STATE: Massachusetts

COUNTRY: USA

ZIP: 02354

## COMPUTER READABLE FORM:

MEDIUM TYPE: CD/ROM ISO9660

COMPUTER: &lt;Unknown&gt;

OPERATING SYSTEM: &lt;Unknown&gt;

SOFTWARE: &lt;Unknown&gt;

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/617,320

FILING DATE: 10-JUL-2003

## PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US/09/107,433

FILING DATE: 30-JUN-1998

APPLICATION NUMBER: 60/ 085131

FILING DATE: MAY 12, 1998

APPLICATION NUMBER: 60/051553

FILING DATE: JULY 2, 1997

## ATTORNEY/AGENT INFORMATION:

NAME: Almeliel, Pamela Dencke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-011

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)899-5007

TELEFAX: (781)893-8277

## INFORMATION FOR SEQ ID NO: 3676:

SEQUENCE CHARACTERISTICS:

LENGTH: 1769 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES

ORIGINAL SOURCE:

ORGANISM: Streptococcus pneumoniae

## FEATURE:

NAME/KEY: misc-feature

LOCATION: (B) LOCATION 1..1769

## SEQUENCE DESCRIPTION: SEQ ID NO: 3676:

US-10-617-320-3676

## RESULT 4

US-10-33-002-19

; Sequence 19, Application US/10333002

; GENERAL INFORMATION:

; APPLICANT: Adderson, Elisabeth

; APPLICANT: Bohnsack, John

; TITLE OF INVENTION: Group B Streptococcus Polypeptides Nucleic Acids and Therapeut

; FILE REFERENCE: 2511-1-001 (SJ-0039)

; CURRENT APPLICATION NUMBER: US/10/333,002

; PRIORITY APPLICATION NUMBER: PCT/US01/24795

; PRIORITY FILING DATE: 2001-08-08

; PRIORITY APPLICATION NUMBER: US 09/634,341

; PRIORITY FILING DATE: 2000-08-08

; NUMBER OF SEQ ID NOS: 37

; SOFTWARE: Patentin version 3.1

; SEQ ID NO: 19

; LENGTH: 560

; TYPE: PRT

; ORGANISM: Streptococcus agalactiae

; US-10-33-002-19

## RESULT 4

US-10-33-002-19

; Sequence 19, Application US/10333002

; GENERAL INFORMATION:

; APPLICANT: Adderson, Elisabeth

; APPLICANT: Bohnsack, John

; TITLE OF INVENTION: Group B Streptococcus Polypeptides Nucleic Acids and Therapeut

; FILE REFERENCE: 2511-1-001 (SJ-0039)

; CURRENT APPLICATION NUMBER: US/10/333,002

; PRIORITY APPLICATION NUMBER: PCT/US01/24795

; PRIORITY FILING DATE: 2001-08-08

; PRIORITY APPLICATION NUMBER: US 09/634,341

; PRIORITY FILING DATE: 2000-08-08

; NUMBER OF SEQ ID NOS: 37

; SOFTWARE: Patentin version 3.1

; SEQ ID NO: 19

; LENGTH: 560

; TYPE: PRT

; ORGANISM: Streptococcus agalactiae

; US-10-33-002-19

## Query Match 3 4%; Score 134; DB 6; Length 1769;

Best Local Similarity 18 6%; Pred. No. 0.34; Mismatches 43;

Matches 161; Conservative 112; Mismatches 268; Indels 325; Gaps 43;

OY 145 RITGDELNQL-LRAVN--YNGHP---QANQIMEGLEPLNAIRVQEA 187

::: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Db 330 KVYDPIQSKVLKAVIDQAAPRVEYTLNGLTPGOVQFNQVF--INNHRITPE-V 383

OY 188 WYSSDNAPATNPDPESFKRESESNLVS--TSQSLSMRQAL---KQLIDPNLATMPKQV 240

::: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Db 384 TYKKINE--TAAEYLMKLDRAHDLNMAETVRLQVVDVNLQHFDVTRIVNQVT--PGQ 439

OY 241 PDDFQ-----LSEFESEDKGDKTNKGIONLLSGLGVPTKPPGDPMPNQP 288

::: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Db 440 IDDERKLSSISFLGNALVSSDGTAKED-----GATMSNNTHSGDDHHDVTPN 491

::: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

OY 289 OTTSVILRKVAGYDVS--KILEGATIQLT---GDN---VNSFOARVSSNDIG--- 333

::: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Db 492 MKD--LAKGMYGFVSTDKLAAGWVNSNSQSYGGSSNDWTRLTAVKETVGNANYGISS 549

::: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

OY 334 -----RRIELSDGTYLTE--LNSPACYSIAE 358

::: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Db 550 EWQWEKAYKGIVFPEYTKELPSAKVWITTEDANADKRVWDQDGALAYRSIMNPQWEVK 609

::: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

OY 359 PITKVEAGYVITI--DGKQIENP-----NKEIVVPSVSEAVND- 396

::: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Db 610 DIT-----AYRIMANFGSQAQNFPLMLDGKIKNLHTDGLGQGVLKQYGSSEGHDSG 662

::: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

OY 397 -----FEEFSVLTQNYAKFY-----YAKNKNGSSQQVVCNFNAD 430

::: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Db 663 HLNYADIGKRIGGVDFEKTIEK--AKYGAHLGIVHNASETYPSKYNEKIL----- 714

QY 431 LKSPPDSESGCKTMTPDFTEGVKTHAGR---DLFKVTKPRD-----T 473

Db 715 RKNPDPSSYIOWNWLDQGINIDAADLDAHGLRALARWEDKKLKGQSLDFTWVNGQSG 774

QY 474 DPDTEFKHI--KKVLEKGYR---EGQQA-----IEVSLGLTEVQLRANTQALI 515

Db 775 DNGARATHVLAKEINKWRFIAENGHGEYDSTFHWAADLTQYGTQNGKINSATRFI 834

QY 516 YYFTDSR-----ELKDKLADYHGGDMND---SLAVAKILYEAQ 554

Db 835 RHNHQKAWVGYDGRYSGAANYPLGGYSGMDFEGQGRSDYQSGYVNLFAHDWVMTQFQH 894

QY 555 -----DSNPQIOLDFLFTPPNNKYOSLIGTQHONHPELDVLDIIRMEDKEV-----PV 602

Db 895 FTVSKRNENGTFPTVMD-----NGSY-----KTPPEMVELUDNNKRVWTKSNDV 942

QY 603 THNLTLRKVT-----GLAGDRPKDFEIEKLKNKNGEL--- 636

Db 943 NSPLYRERTVTYLNGRVQDASLYTPWWDANGKKLSTDKEKMYFNTQAGATWTLPSD 1002

QY 637 -----LSQTWVTDKTRLEFRKGATNLKQSLTQGLPDBGSYLVKED--- 682

Db 1003 WAKSKVLYKTDQGKTEQEQLTVKGKTDILANQPVYL-----YRSKQINPEMS 1054

QY 683 -SEG--YKVVKNSQEVANATV--SKGTG-----SDTLEAFENKEPV----- 720

Db 1055 WSEGMIYIDQGFNSTLKHWTISGASKAERVKSQGANDMRIGRSNEKVKSLQTLGLK 1114

QY 721 -----VPTGTDQKTYGLATIVIG 740

Db 1115 PNTKAVYVGVDNRNSAKASITVNG 1140





```

; SOFTWARE: Patentin version 3.2
; SEQ ID NO: 1651
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-60-890-1651

Query Match 3 3%; Score 129; DB 7; Length 461;
Best Local Similarity 19 7%; Pred. No. 0.12; Mismatches 232; Indels 256; Gaps 35;
Matches 91; Conservative 82; Mismatches 170; Indels 118; Gaps 24;

Qy 275 PPTPGDPPMP---PNQPORTSVLIR--R-KYAGDYSKLEGATEFQLTGDNVNSFOARVF 327
Db 35 PALPKPKPKPTSAPNGMKDSSVSLQDAEWYWDISR---EVENDKLDRMPDGIF 87
Qy 328 SSNDIGERISLSDGTYLT-----ELNSPAGYSIAEPTFVKEAGKVYIIDGK 376
Db 88 LVRDASTKMQ--GDTLTLURGGNNKLKLYIHRDGKYSFSDPLIF---NSVVELINHY 140
Qy 377 QIE-----NPNKETVEPVSYEAYND--FEFSVLTQVAKFYAKNNKNGSSQVYCFN 428
Db 141 HHESLAQYNPRLKDVKLYMVPYSRYQODQVLKDNDIAVGKQLQEVHSQYQBSKEYDRLYE 200
Qy 429 ADLSPPPDSEGGKTMTPDFTGEVKYTHAGRDLFKYVPRDDPDTFLKHKKVIEK 488
Db 201 EYTRSQEI-----QMKRTAI--EAENETKIFERQHCOEQHSKEYIER 243
Qy 489 GYREKGQATEYSGLTETQRAATOLAIYVFTDSAELDKLKDVGFGMDNSTAVAKI 548
Db 244 -FRREGNEKEERIM-----MYDKLKS--RIGEHDHSKRLED 280
Qy 549 LVEYADSDNPQPLDDEFIPNNKKYQSLIGTQWHPEDVDIRMEDKEVTPVHNLTL 608
Db 281 LKKQALDNR---EID---KMNST-----KPDLIQLRKIRD-OHLVWLHK-- 319
Qy 609 RKTIVGLAGRTKDFEETEIKNNKKQELLSQTVKTDKTNLEFKOGKA---TINHKGES 664
Db 320 -----GYRQKRNUWVGLKINED-ENYFINEDEENLPHYDFTWVFEDINRVOAED 370
Qy 665 LTQGLPSEGYSVLYKETDEB-G-YKVYUNSO-EVANATVSK 703
Db 371 L-LIGKPDG-AFLIRESSKKGCYACSVVADGEVVKCVIIST 409

RESULT 9
US-10-286-897-2582
; Sequence 2582, Application US/10286897
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 74FLPCT
; CURRENT APPLICATION NUMBER: US/10/286, 897
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US/09/488, 725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US/09/552, 317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US/09/598, 042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US/09/620, 312
; PRIOR APPLICATION NUMBER: US/09/653, 450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US/09/662, 191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US/09/693, 036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US/09/727, 344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7143
; SOFTWARE: pt_FL_genes_b Versions 1.0
; SEQ ID NO: 2582
; LENGTH: 993

; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-286-897-2582
; Sequence 2582, Application US/10286897
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 74FLPCT
; CURRENT APPLICATION NUMBER: US/10/258, 898A
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US/09/488, 725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US/09/552, 317
; PRIOR APPLICATION NUMBER: US/09/620, 312
; PRIOR APPLICATION NUMBER: US/09/653, 450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US/09/662, 191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US/09/693, 036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US/09/727, 344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7143
; SOFTWARE: pt_FL_genes_b Versions 1.0
; SEQ ID NO: 2582
; LENGTH: 993

Query Match 3 2%; Score 128; DB 6; Length 993;
Best Local Similarity 20 1%; Pred. No. 0.43; Mismatches 232; Indels 256; Gaps 35;
Matches 145; Conservative 89; Mismatches 232; Indels 256; Gaps 35;

Qy 85 YKQFRVAHDLR--VILE-GSRSYOVYCFNLUKKAFL--GSDSSVKKWYKHDGISTKE 138
Db 76 EYCRSPN-----EFAQHAPKEVKVNUKOCCECNKE-----IKVRE-----N 113
Qy 199 PDE-SFKRESESNIVLTSQSLSMRQ-ALKQOLIDPLATKMPQVPPDDQLSFESEDKG 255
Db 114 ETEIQEIKMEEERNLIPREEKPIEIERKENTKPSLGK----- 153
Qy 256 DKYNQGYONLISGGIYVPTKPPGPPMPNPQPTSVLIRKYAIGDYSKLEGATLQLT 315
Db 154 -----KNILES-----IPHSQDEKEVNIK-----P 175
Qy 316 GDNVNFSQARVFSSNDIGERIELSGTLYTTELSPAGYSIAETTEKVYAGKVYIING 375
Db 176 EDNEN-----LDDDDDTTRVD-----ESLNKIVYAEEE---KA 206
Qy 376 KOIERNPK-----EIVEPVSYEAYNDFEFSVLTQVAKFYAKNNKNG 419
Db 207 KSGDFTPNEEDEDDESEAAEEEEEDEDDDDNNEEEFECYPPGMVKVQVRGKNN- 265
Qy 420 SSQVYVCFNADLKSPPDSEGGKTMTPDFTGEVKY-TTAGDLFY-----TVPK 470
Db 266 -OQMY--ERSIK---DSDEVG-----GEVILVLYCWWN-RYDEWIKADKIVRP 309
Qy 471 RDTDDTFLHKKYIEKGREKQSAIEGLTETOLRAATOLAIYVFTDSAELDKLKK 530
Db 309 ADKNYPK-IKHKRKKNNKLKDKEKDKEYKSP-KNCKFLR-----RLSKPFFQ 352
Qy 531 DYHGGDMNSTLAVAKILVEYADSDNPQPLDFFINNNKKYQSLIGTQWHPEDLYI 590
Db 353 -----TNPSPEMVSKLDLTDAKNSTDTHAKSIE-----TSLINGQASSEAAED 397
Qy 591 IRMEDKEKEVIFVTHNLTLRKTVTGLAGDRKDFHEETEIKNNKKQELLSOTVKTDRKNEF 650
Db 398 SEQERGAGDMNL-----GKEESKIDH-----LTNNRNDLISKEQNSSLLIE 443
Qy 651 RDGKATINTLKHGESTLTOGLQPEPEGYSVLYKETDSGGYKVUNSOVANAVS----- 701
Db 444 NKVHADLVLISKPVSKSPERLRKDIEVLSIDYEDDEVIKRKWDKDTDKSSKPKQIKR 503
Qy 702 -----KTC-----ITSDETLAFENN-----KPVVPGDQKI 729
Db 504 GKRYYCNETECKTGTSPGKKEEKAKNKECLMCNNSNSSSDEDDEETAKMPT--KYY 560
Qy 730 NG 731
Db 561 NG 562

RESULT 10
US-10-258-898A-2582
; Sequence 2582, Application US/10258898A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 74FLPCT
; CURRENT APPLICATION NUMBER: US/10/258, 898A
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US/09/488, 725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US/09/552, 317
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US/09/620, 312
; PRIOR APPLICATION NUMBER: US/09/653, 450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US/09/662, 191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US/09/693, 036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US/09/727, 344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7143
; SOFTWARE: pt_FL_genes_b Versions 1.0
; SEQ ID NO: 2582
; LENGTH: 993

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PRIOR FILING DATE: 2000-04-25  
 PRIOR APPLICATION NUMBER: US09/598,042  
 PRIOR FILING DATE: 2000-06-20  
 PRIOR APPLICATION NUMBER: US09/620,312  
 PRIOR FILING DATE: 2000-07-19  
 PRIOR APPLICATION NUMBER: US09/653,450  
 PRIOR FILING DATE: 2000-08-31  
 PRIOR APPLICATION NUMBER: US09/662,191  
 PRIOR FILING DATE: 2000-09-14  
 PRIOR APPLICATION NUMBER: US09/693,036  
 PRIOR FILING DATE: 2000-10-19  
 PRIOR APPLICATION NUMBER: US09/727,344  
 NUMBER OF SEQ ID NOS: 7143  
 SOFTWARE: pt\_FL\_genes\_b Versions 1.0  
 SEQ ID NO: 2582  
 LENGTH: 993  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-258-89A-2582

Query Match 3.2%; Score 128; DB 6; Length 993;  
 Best Local Similarity 20.1%; Pred. No. 0.43; Mismatches 145; Conservative 89; Indels 232; Gaps 35; Matches 145; Pred. No. 0.43; Mismatches 232; Indels 256; Gaps 35; Db 22 FKLFLRVLKLGFDNIESGAVWKVY--QDYGIPVLSAAGYNVKCYKYY--LYGFE 75

Qy 85 YKQFRYAHDLR--VNLE-GSRSYQVQCFNLKAFPL--GSDSSVWKWKKHDGISTKFE 138  
 Qy 199 PDE--SFKRESNLVSTSQISLMO-ALKQIOLDPNLATKPKQVDDFQLSIFESEDKG 255  
 Db 114 ETEIQLIEKMEBERNIPPREERPLDETERKENIKPSLSK----- 153  
 Qy 256 DKNKGYQONLLSGLGLVPTKPPMPGDPMPNPQQTTSVLRKYAIGDYSKLEGATLQLT 315  
 Db 154 -----KNNLES-----IPIHSDQEKEVENIKK-----P 175  
 Qy 316 GDNVNSFQARVESSNDIGERIELSDGTYTTELNSPAGYSTAEPITFKVEAGKVYI 375  
 Db 176 EDNEN-----LDDKDDTTRVD-----ESLNKVEAEE---KA 206  
 Qy 376 KOIENPNK-----ELVEPYSEAVKDFEEFSVLTQNYAKFYAKNNK 419  
 Db 207 KSGDEKNEEDDEEAEEREEEREDDEDDNNEECYPEPGMKVQYRGKNG- 265  
 Qy 420 SSQVVCFCNADLKSPPDSEDGKTMTPDFTGEVKY-THIAGRDLRY-----TVKP 470  
 Db 266 --QKMY--EASTK--DSDVEG-----GEVLYVHCGWNV-RYDEWIKADEVKIVRP 308  
 Qy 471 RUDTPDPMELKHKVTEGVYERKGQIAEYSGLETQIARAATQALITYFTSAAELDKKLK 530  
 Db 309 ADKVNPK-IKRRKKRNKLDEKDKDKEVSP-KNCKLR-----RLSKPFPQ 352  
 Qy 531 DYHGFDMNDSLAVAKILVEQAQDSNPPQTLDFIPNNKQYOLIGTWHPELDKLK 590  
 Db 353 -----TNPSPMVKLUDTAKNSDTAHKSI-----TSILINGQIQAESSAED 397  
 Qy 591 IRMEDKKEVIVPYTHNLTLRKTVTGLAGDRTKDFHFETELKNKQELLSQTVKTDKTNL 650  
 Db 398 SEQEDERGAQDMNN-----GKEESKDH---LTNNRNDLISKERONSSSLEE 443  
 Qy 651 KDGKATNLKKGESLTLQGLPEGYSYLVKEKDSEGYKVQNSQEVANATVS----- 701  
 Db 444 NVKHADLIVISKPVSKSPERLRKDIEVISEDYEEDEVTKRDKVDDKSSKQIKR 503  
 Qy 702 -----KLG-----ITSEDELAFFN-----KEPVVPTGQDKI 729  
 Db 504 GKRRYCNTECLKTGSPGKKEKAKKNEKSLMENSNSSSDEDEETKAKMPT--KY 560

RESULT 11  
 US-10-408-765A-2576  
 Sequence 2576 Application US/10408765A  
 GENERAL INFORMATION:  
 APPLICANT: Ghosh, Soumitra S.  
 APPLICANT: Fahy, Eoin D.  
 APPLICANT: Zhang, Bing  
 APPLICANT: Gibson, Bradford W.  
 APPLICANT: Taylor, Steven W.  
 APPLICANT: Glenn, Gary M.  
 APPLICANT: Warnock, Dale E.  
 TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
 TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME  
 FILE REFERENCE: 660088 465  
 CURRENT APPLICATION NUMBER: US/10/408,765A  
 CURRENT FILING DATE: 2003-04-04  
 NUMBER OF SEQ ID NOS: 3077  
 SEQ ID NO: 2576  
 LENGTH: 1090  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-408-765A-2576

Query Match 3.2%; Score 128; DB 6; Length 1090;  
 Best Local Similarity 18.3%; Pred. No. 0.49; Mismatches 153; Conservative 125; Indels 278; Gaps 42; Matches 153; Pred. No. 0.49; Mismatches 280; Indels 278; Gaps 42; Db 311 VTPARVERRSVLLIEETVTIN--NSNALSHEFAYGAASESFQGPP-----I 356  
 Qy 97 NLEGRSRYQVQCFNLKAFPLGSDSSVKK---WYKKHDGISTKFEDYAMSPTGDEL 151  
 Db 357 DISTRKKHOILF--KEENP--NNDITVLKGSTANFNKTPSPVAPNVAKATISARFPNLK 413  
 Qy 152 NOKLRAWMYNGHPONANGIMEGLEPLINAIRYQEAWYYSNAPLSNPDSFKEKRSSENLI 211  
 Db 414 KTNLADAL--HSQS-----IIPLEENVIPD-----DNLSTSKDTK-EANRASI 457  
 Qy 212 VTSQSLSLRQALKQIOLDPNLATKPKQVDDFQLSIFESEDKGDKYNGQYQNLSSGL- 270  
 Db 458 IFTS---MNECTSTVDTVSPVSTESVSYVSDML--PGD--NYKSRGSDRNL 508  
 Qy 271 -----VPTKRPPTGDPMPNPQQTTSVLRKYAIGDYSKLEGATL--QDYGIPVLSAAGY 323  
 Db 509 LLDSLNENPTEPG--LMRDNSFSESSI-----TRSEELERATEVGAINGGNYPEKQ 558  
 Qy 324 ARVFSN---DIGERIELSDGTYTTELNSPAGYSTA---EPITFKVEAGKVY----- 371  
 Db 559 VLTQTNHSYPLAWQVSPPIESTFSNNPTDSBINFESFSFSPVNGNTPGNGETDEIVSKRSQR 618  
 Qy 372 -----IITDGKQ----- 377  
 Db 619 AIEKAFSQIKESONSYVKIRKILANSQEDPATMFKLHSHTNTTVLIPAIWKIPPSATKL 678  
 Qy 378 --IENPNKEIVEPYSV-EAYNDFEE-----FSVLTQNYAKFYAKNNQYQVY 425  
 Db 679 NLLNSNSDSDVDEEFHSEAGNSFSEPSLTSKLQDFSKSQAPPNLKGJSSVY 738  
 Qy 426 CENADLKSPPDSEGD-----GKTMTP-----DFTG-----EV 453  
 Db 739 TSTLSEASRPNDQSSAFHIVSYNTGRSSNTTPARLHGLQWRPTLPSDFTSMADPIYEL 798  
 Qy 454 KYTHIAGRDLFK--YIVKPROT-----DPDFLHKVVKYEGYR 491  
 Db 799 TPTVIMGRDITKRDIFSLPPEETIPSQDVTLPITITSENMSMASTKEFNK-HKDFI 856



783 SPLQAKLAPVITGINSKLEGRFF---GKGFQSHSADKREILAPFPVRD---ETP 834

401 S-----VLTNTQYAKFYAK-----NKNGSSQVVVCFNADLKSPPD- 436

QY 835 GNTALLIKKAESGECOLSTONLIOMAEDSHPLDPTSQLSRKGFS----GDVASPOD 887

QY 437 -----SEDGKTMTP----DFTT----GEVKVTHIAGR 462

Db 888 MLFPQDAHLVPOARVIPSQTESETVKEVILPPRVLNDVSAALQKLGEGWVLSYBAGRE 947

QY 463 LFKYTWKPRDTDPFLKHKVIEKGYREKGQAEYSGLTEROLRAATOLATIYFTDSA 522

QY 948 -----VGPGEPNPE-FPEAVQVC-----SPLNPPGVISPMATMDT 983

Db 523 ELDKDKLKDYGFGDMNDSTLAVAKLVEYAOQDSNPQLTDLDFPNNKYSOLGT-- 580

QY 984 VPDR---KDFYSSNNVPDKTHEVGSYL---AQMSPSDOT-----LSSEASIVAOQY 1029

QY 581 QWHPEDLVDIIRMEDKKEVIPVTHNLTRKTVGLAGDRKDF-HFETELNK-NKQELL 637

Db 1030 KGLPQVEEIVR---ETVOPRSEFLFESAGLKLKETEFPSKVESDTGNISPSKJ 1086

QY 638 SQTVKTDKTNLF--KDGKATNLKKGESLTQGLPEGSYLVE-TDSEGKVVKNSOE 694

QY 1087 GSTEERRRATSECHPEELKETWEKAAPLITESAFDAGEFKLKEITEPAPYQOQNSRE 1146

QY 695 VANATVSKTGITSDET 710

Db 1147 ---ETHEKESSESEQT 1159

RESULT 14

US-09-200-650E-3

Sequence 3, Application US/09200650E

GENERAL INFORMATION:

APPLICANT: Patti, Joseph M.

APPLICANT: Foster, Timothy J.

APPLICANT: Hook, Magnus A.O.

APPLICANT: Deirdre Ni

APPLICANT: Perkins, Samuel L.

TITLE OF INVENTION: Extracellular Matrix-Binding Proteins from *Staphylococcus aureus*

FILE REFERENCE: 05283US2/BAS

CURRENT APPLICATION NUMBER: US/09/200.650E

CURRENT FILING DATE: 1998-11-25

PRIOR APPLICATION NUMBER: 60-066, 815

PRIOR FILING DATE: 1997-11-26

PRIOR APPLICATION NUMBER: 60-098, 427

PRIOR FILING DATE: 1998-08-31

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3

LENGTH: 930

TYPE: PRT

ORGANISM: *Staphylococcus aureus*

US-09-200-650E-3

Query Match 3.2%; Score 125.5; DB 5; Length 930;

Best Local Similarity 19.4%; Pred. No. 0.59; Matches 115; Conservative 71; Mismatches 215; Indels 193; Gaps 26;

QY 183 TQEAWWYSDNAPISNIDESFRKREESLNVLSTSQQSLMRQALKQLIDPMLATKMPKQVDP 242

Db 86 TQET-----ADQPKVMSDATVKETSSNMQSPONATANOS-----TTKISSNVTN 132

QY 243 DFLSLTSESEDKGDKYKNGYQNLISGGLVPTKPTPGDPPMPPNQOPRTSVLTKYATGD 302

Db 133 DKSSTTIVSNET---DK----SNITOKAVDSTPKTTKPTKRTKPTLNRMAVNVAADQ---- 180

QY 303 YSKLLEGATLQLTGDNVNSFQARV-FSSNDIGERIELSDGTIVTLE-----LNSPAG 353

Db 181 -----QGTNYND---KVHFSNDIAIDKGHNOTICKTEFWATSSDVLKLN 225

QY 354 YSIAEPI-----TFK---VERAGKVTITDQGQIENENKEVIEPVSYAVNDTEESVLY 403

226 YLTDDSVREGIDTFKQYQFRRPGSVRLPSQTONLYNAQGNTI--AKGIVDSTTNTM 282

Db 404 TTONYAKFY-----YAKNKGSS-QVYCFNADLKSPDSE---GGKTMTP 446

Db 283 TFTNIVQYQTYNRGSFSEQVAFAKRKNATDCKTAKYMEVTLGNDTYSEELIVDGNKKAQ 342

QY 447 DFTTGEVKVTHIAGRDFKTYWKPRDT-DPDPFLKHKVIEKGYREKGQAEYSGLTER 505

Db 343 LISSTNYINNEDLSRNNTAYVNQPKNTYTKTQFTVNL---TGKFENPNANKF 392

QY 506 QIRATOLATIYFTDSAELDKKLKDYGFGDMNDSTLAVAKLVEYAOQDSNPQLTD 555

Db 393 -----IYEVTDQNOF-----VD 404

QY 566 FFPNNNNYQSLIGTQWHPELDVITRNMEDKKEVIPVTHNLTRKTVGLAGDRKDFH 625

Db 405 SFTPDISKLUKV-----TQFDVIVSNDK---TATVDLMKQG----- 440

QY 626 EELKNUKKQELSO-----TVEKDKTNUFKOGKATNLKKGESLTQGL 669

Db 441 ---SSNKQYIQQAVPDNNSSTDNGKIDYDIDKTKYWSNSYNSN-----GSSTANG 492

QY 670 LPEGYS---YVYKETDSEGKVVKVNSQEVANAV--SKTGITSDETAFENK 717

Db 493 DOKKYNLGDYWDNTNKG-KODANEKGKGVVYVILKDSNGKELDRTT'DENGK 545

RESULT 15

US-10-617-320-3251

Sequence 3251, Application US/10617320

GENERAL INFORMATION:

APPLICANT: Lynn A. Doucette-Stamm and David Bush

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO *STREPTOCOCUS PNEUMONIAE* FOR DI

CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street

CITY: Waltham

STATE: Massachusetts

COUNTRY: USA

ZIP: 02354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD/ROM ISO9660

COMPUTER: <Unknown>

OPERATING SYSTEM: <Unknown>

SOFTWARE: <Unknown>

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/617, 320

FILING DATE: 10-JUL-2003

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/107, 433

FILING DATE: 30-Jun-1998

APPLICATION NUMBER: 60/ 085131

FILING DATE: May 12, 1998

APPLICATION NUMBER: 60-051553

ATTORNEY/AGENT INFORMATION:

NAME: Arinieillo, Pamela Deniske

REGISTRATION NUMBER: 40, 489

REFERENCE/DOCKET NUMBER: GTC-011

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 3251:

SEQUENCE CHARACTERISTICS:

LENGTH: 1972 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES

ORIGINAL SOURCE: Streptococcus pneumoniae  
ORGANISM: Streptococcus pneumoniae  
FEATURE: misc\_feature  
NAME/KEY: misc\_feature  
LOCATION: (B) LOCATION 1..1972  
SEQUENCE DESCRIPTION: SEQ ID NO: 3251:  
US-10-617-320-3251

Search completed: August 19, 2003, 15:29:15  
Job time : 40 secs